

4 pgs SEG. List

Table 6

CD28TFc sequence (SEQ ID NO:2)

(thrombin site separating the two halves of the chimera is shown in bold)

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1  CCCCATCCGCTCAAGCAGGCCACCATGGATTGGCTGCGGAACTTGCTATTCCTGATGGCG
   -----+-----+-----+-----+-----+-----+ 60
   GGGGTAGGCGAGTTCGTCCGGTGGTACCTAACCGACGCCTTGAACGATAAGGACTACCGC
a      M D W L R N L L F L M A -

61  GCCGCTCAAAGTATCAACGCGAACAAGATCTTGGTGAAGCAGTCGCCCATGCTTGTAGCG
   -----+-----+-----+-----+-----+-----+ 120
   CGGCGAGTTTCATAGTTGCGCTTGTCTAGAACCACTTCGTGAGCGGGTACGAACATCGC
a      A A Q S I N A N K I L V K Q S P M L V A -

121 TACGACAATGCGGTCAACCTTAGCTGCAAGTATTCCTACAATCTCTTCTCAAGGGAGTTC
   -----+-----+-----+-----+-----+-----+ 180
   ATGCTGTTACGCCAGTTGGAATCGACGTTTCATAAGGATGTTAGAGAAGAGTTCCTCAAG
a      Y D N A V N L S C K Y S Y N L F S R E F -

181 CGGGCATCCCTTCACAAAGGACTGGATAGTCTGTGGAAGTCTGTGTTGTATATGGGAAT
   -----+-----+-----+-----+-----+-----+ 240
   GCCCGTAGGGGAAGTGTTTCCTGACCTATCACGACACCTTCAGACACAACATATACCCTTA
a      R A S L H K G L D S A V E V C V V Y G N -

241 TACTCCCAGCAGCTTCAGGTTTACTCAAAAACGGGGTTCAACTGTGATGGGAAATTGGGC
   -----+-----+-----+-----+-----+-----+ 300
   ATGAGGGTTCGTCTGAAGTCCAAATGAGTTTTTGCCCCAAGTTGACACTACCCTTTAACCCG
a      Y S Q Q L Q V Y S K T G F N C D G K L G -

301 AATGAATCAGTGACATTCTACCTCCAGAATTTGTATGTTAACCAAACAGATATTTACTTC
   -----+-----+-----+-----+-----+-----+ 360
   TTACTTAGTCACTGTAAGATGGAGGTCTTAAACATACAATTGGTTTGTCTATAAATGAAG
a      N E S V T F Y L Q N L Y V N Q T D I Y F -
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361 TGCAAAATTGAAGTTATGTATCCTCCTTACCTAGACAATGAGAAGAGCAATGGTACC 420
-----+-----+-----+-----+-----+-----+
ACGTTTAACTTCAATACATAGGAGGAGGAATGGATCTGTTACTCTTCTCGTTACCATGG
a C K I E V M Y P P P Y L D N E K S N G T -

421 ATTATCCATGTGAAAGGGAAACACCTTTGTCCAAGTCCGCTATTTCCCGGACCTTCTAAG 480
-----+-----+-----+-----+-----+-----+
TAATAGGTACACTTTCCTTTGTGGAACAGGTTCAAGGCGATAAAGGGCCTGGAAGATTCT
a I I H V K G K H L C P S P L F P G P S K -

481 CCCCTGGTACCCAGGGGTAGTGGTAGTAAGCCTAGCATAAGTACAGTCCCAGAAGTATCA 540
-----+-----+-----+-----+-----+-----+
GGGGACCATGGGTCCCCATCACCATCATTTCGGATCGTATTCATGTCAGGGTCTTCATAGT
a P L V P R G S G S K P S I S T V P E V S -

541 TCTGTCTTCATCTTCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAG 600
-----+-----+-----+-----+-----+-----+
AGACAGAAGTAGAAGGGGGGTTTCGGGTTCTACACGAGTGGTAATGAGACTGAGGATTC
a S V F I F P P K P K D V L T I T L T P K -

601 GTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTT 660
-----+-----+-----+-----+-----+-----+
CAGTGCACACAACACCATCTGTAGTCGTTCTTACTAGGGCTCCAGGTCAAGTCGACCAAA
a V T C V V V D I S K D D P E V Q F S W F -

661 GTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACCCGGGAGGAGCAGTTCAACAGC 720
-----+-----+-----+-----+-----+-----+
CATCTACTACACCTCCACGTGTGTGCGAGTCTGCGTTGGGGCCCTCCTCGTCAAGTTGTCTG
a V D D V E V H T A Q T Q P R E E Q F N S -

721 ACTTTCCGCTCAGTCAGTGAAC TTCCCATCATGCACCAGGACTGGCTCAATGGCAAGGAG 780
-----+-----+-----+-----+-----+-----+
TGAAAGGCGAGTCAGTCAC TTGAAGGGTAGTACGTGGTCCTGACCGAGTTACCGTTCCTC
a T F R S V S E L P I M H Q D W L N G K E -

781 TTCAAATGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCCATCGAGAAAACCATCTCCAAA 840
-----+-----+-----+-----+-----+-----+
AAGTTTACGTCCCAGTTGT CACGTGAAAGGGACGGGGGTAGCTCTTTTGGTAGAGGTTT
a F K C R V N S A A F P A P I E K T I S K -

841 ACCAAAGGCAGACCGAAGGCTCCACAGGTGTACACCATTCACCTCCCAAGGAGCAGATG 900
-----+-----+-----+-----+-----+-----+
TGGTTTCCGTCTGGCTTCC GAGGTGTCCACATGTGGTAAGGTGGAGGGTTCTCTGTCTAC
a T K G R P K A P Q V Y T I P P P K E Q M -

901 GCCAAGGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAGACATTACT 960
-----+-----+-----+-----+-----+-----+
CGGTTCTCTATTTTCAGT CAGACTGGACGTACTATTGTCTGAAGAAGGGACTTCTGTAATGA
a A K D K V S L T C M I T D F F P E D I T -

961 GTGGAGTGGCAGTGGAAATGGGCAGCCAGCGGAGAACTACAAGAACACTCAGCCCATCATG 1020
-----+-----+-----+-----+-----+-----+
CACCTCACCGTCACCTTAC CCGTCGGTCGCCTCTTGATGTTCTTGTGAGTCGGGTAGTAC
a V E W Q W N G Q P A E N Y K N T Q P I M -

1021 GACACAGATGGCTCTTACTTCGTCTACAGCAAGCTCAATGTGCAGAAGAGCAACTGGGAG 1080
-----+-----+-----+-----+-----+-----+
CTGTGTCTACCGAGAATGA AGCAGATGTCGTTGAGTTACACGTCTTCTCGTTGACCCTC
a D T D G S Y F V Y S K L N V Q K S N W E -

120

1081 GCAGGAAATACTTTACCTGCTCTGTGTTACATGAGGGCCTGCACAACCACCATACTGAG
-----+-----+-----+-----+-----+ 1140
CGTCCTTTATGAAAGTGGACGAGACACAATGTACTCCCGGACGTGTTGGTGCTATGACTC

a A G N T F T C S V L H E G L H N H H T E -

AAGAGCCTCTCCCACTCTCCTGGTAAATAA
1141 -----+-----+-----+ 1170
TTCTCGGAGAGGGTGAGAGGACCATTATT

a K S L S H S P G K * -